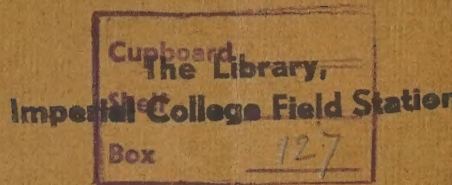


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A SEX-LINKED TRANSLUCENT GENE WHICH OCCURRED
INDEPENDENTLY IN THREE DIFFERENT
STRAINS OF THE SILKWORM¹

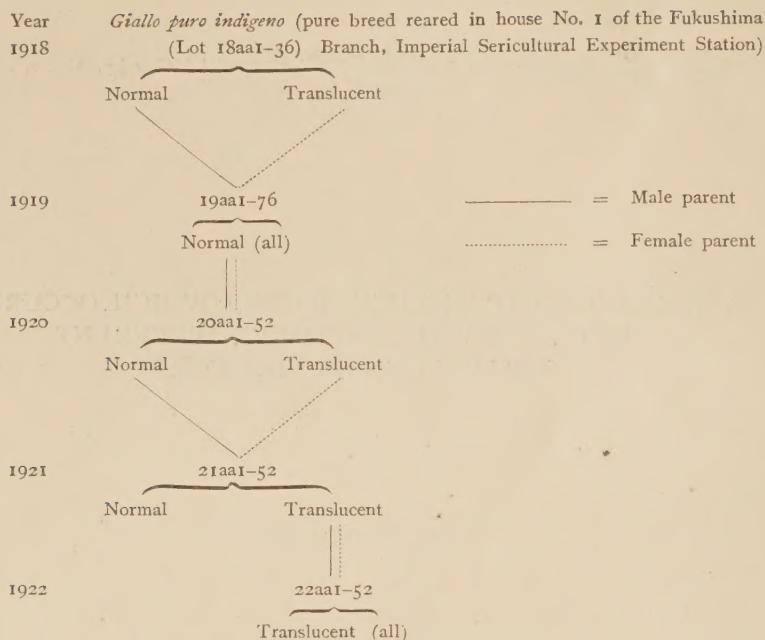
Yoshimaro TANAKA

I have observed silkworm larvae with translucent skin due to a single recessive gene *os*, an allelomorph to the normal gene *Os*, in three unrelated strains. They are described in the present paper.

I. *GIALLO-PURO* TRANSLUCENT

In 1916, I discovered translucent larvae in F₁ generation of a cross between Japanese bivoltine *Okusa* and Italian univoltine *Giallo puro indigeno*, the translucent character of which was sex-linked in inheritance, and the symbol *os* was adopted for that gene. Later I found *os*-translucent in the pure breed of *Giallo puro*, but never in pure *Okusa*, hence it is certain that the *os* gene was brought in our *Giallo puro* breed. The pedigree of the pure *os*-strain which we are keeping up to the present is given below.

¹ Contributions from the Sericultural Laboratory, Kyushu Imperial University, No. 8.



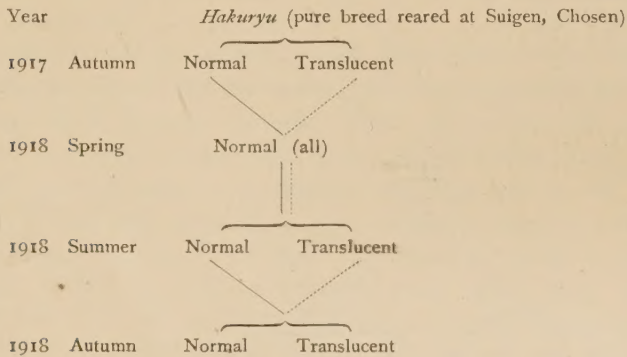
The sex-linked transluents from *Giallo puro* are homozygous for blood and cocoon colors (yellow), voltinism (univoltine) and molting character (4-molters, i. e. they pass through four molts before spinning cocoons). But they are considerably variable in marking intensity, showing every grade from no-marking (plain) to moderately dark normal marking. More detailed descriptions of this strain are to be found in my previous papers (TANAKA 1917, 1922).

II. HAKURYU TRANSLUCENT

H. NISHIKAWA, geneticist in the Sericultural Experiment Station, Suigen, Chosen (= Korea), has reported another strain of sex-linked transluents from a pure Japanese breed *Hakuryu* (NISHIKAWA 1918, 1922). This race was homozygous bivoltine, white-blooded, normal or quail-marked, 4-molters.

Through the kindness of Mr. NISHIKAWA, I received the eggs of *Hakuryu* translucent in exchange for those of my *Giallo puro* strain. I crossed the two under consideration and obtained only translucent F_1 larvae, proving that *Hakuryu* translucent is due to the same gene as

Giallo puro translucent. According to Mr. NISHIKAWA, his strain originated from two translucent larvae (both female) discovered in the autumnal culture 1917 in a pure breed of *Hakuryu* and crossed with their normal opaque brothers. The pedigree is as follows:

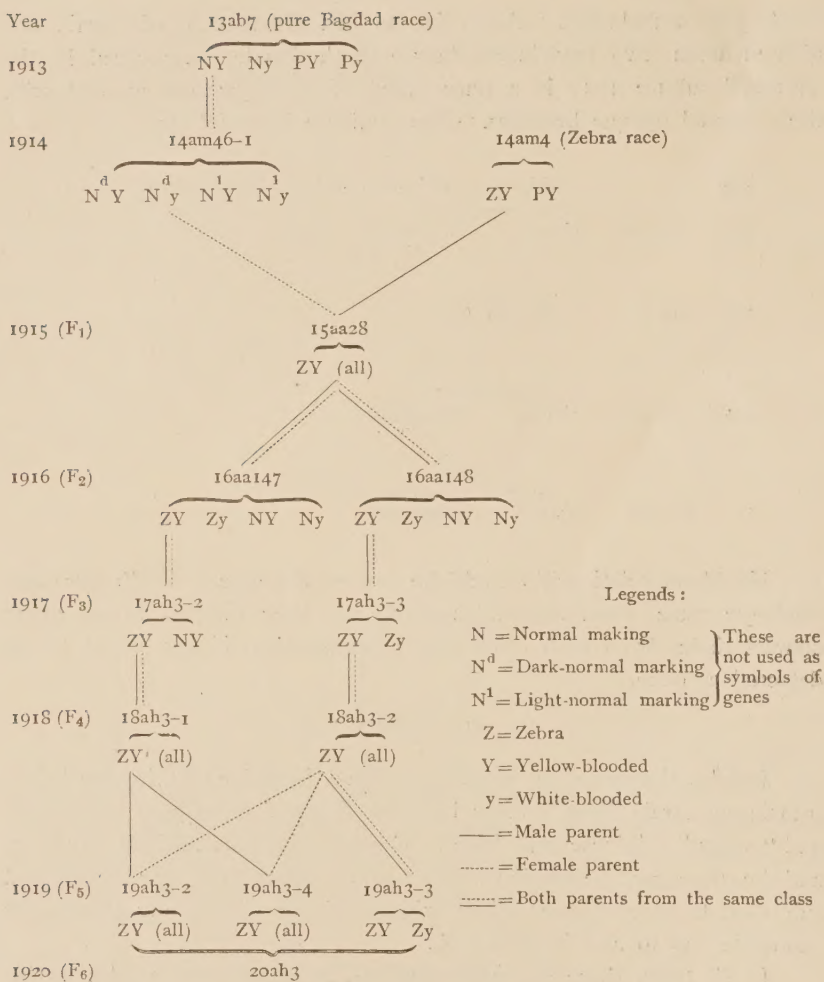


No blood relationship could be suspected between *Giallo puro* and *Hakuryu* reared thousands miles apart, and they differed in so many characteristics from each other that contamination, if any, ought to be detected at once.

III. H_3 TRANSLUCENT

Besides the two cases mentioned above, I obtained a third sex-linked translucent strain from a cross between *Bagdad* (European univoltine) and "zebra" (Chinese univoltine). F_1 generation was cultivated in 1914, and the subsequent generations, mated among themselves, were reared and subjected to careful observations without giving rise to any translucent caterpillar up to and including F_5 .

In F_6 1920, there suddenly appeared 26 translucent females in this strain, lot 20ah3, whose pedigree is shown below.



The segregation in lot 20ah3 was as follows:

	Opaque (normal)		Translucent		Totals
	♀	♂	♀	♂	
Zebra, yellow-blooded	178	292	19	0	489
Zebra, white-blooded	58	77	7	0	142
Totals	236	369	26	0	631

This lot was a mixed culture of larvae from 21 batches, and consequently the proportion of translucent to opaque has little significance. Nevertheless the extremely small number of translucent in this lot could be taken to suggest that the translucent larvae appeared in only one or at most a few of the batches reared.

I have bred a new translucent strain from the offspring of translucent females mentioned above by mating them to normal brothers. Crossing was made between this translucent strain and that of *Giallo puro* as well as that of *Hakuryu*. The offspring were all translucent in either cross, i. e. the *h3*-translucent was also due to *os* gene as in the case of the other two strains.

Although we had already *Giallo puro* translucent in our possession when *h3*-translucent females made their first appearance, no contamination was likely to occur between them. If mating had taken place between *h3*-opaque females and *Giallo puro* translucent males in F_5 , 1919, it would have resulted in segregation of opaque males and translucent females in the next generation, 1920, giving no translucent males as was actually the case. But if this generation were produced in such a way it ought to have consisted of yellow-blooded larvae only, because the *Giallo puro* race was homozygous yellow, whereas the actual result was contrary to this expectation; we had both yellow and white blooded larvae in translucent type as well as in opaque.

No other way of contamination which might give rise to translucent females but no translucent males, could be imagined. Suppose, for example, contamination had occurred between still more remote ancestors, say between translucent females (*Giallo*) and opaque (*h3*) males in F_4 . In that case the normal marking or plain character of *Giallo* must have segregated in F_6 . But this was not actually the case.

IV. SUMMARY

The sex-linked translucent gene *os* has occurred independently in three different races of silkworm, *Giallo puro*, *Hakuryu* and *h3*. The first two were pure races, while the last one was a hybrid strain. This is an example of parallel mutation in the silkworm.

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“STICK” AND “MULTILUNAR,” A FOURTH LINKAGE GROUP IN THE SILKWORM¹

Yoshimaro TANAKA and Seiichi MATSUNO

I. ORIGIN OF “STICK”

Among 121 larvae in a lot, No.193 p95-1, reared in the third season 1919, 10 caterpillars were found to be abnormal. They had rather small and slender body, exceedingly stiff in touch. The pedigree of this family had been exactly known for more than twelve generations, each generation being subjected to minute observation, and no similar occurrence in any previous generation was recorded. The pedigree is given in the Table 1.

Table 1

131x9 (Japanese bivoltine, 4m, marking pale quail, cocoon white, eggs purple)	131M14-1 (Chinese univoltine, 3m, marking plain, cocoon yellow, eggs blue)
 141A11	 141M37
 142A22	
 151A99	 151A17
♀	♂
×	

¹ Contributions from the Sericultural Laboratory, Kyushu Imperial University, No. 9. The experiments were made at the Fukushima Branch of the Imperial Sericultural Experiment Station up to 1922, since then at our university.

152A382	plain, yellow, 3m.	(1)
161A316	plain, yellow and white, 3m.	(1)
162p6	plain, yellow, 3m.	(3)
171p95-I	plain, yellow, 3m.	(4)
172p95-I	plain, yellow	(5)
181p95-I	" "	(12)
182p95-I	" "	(8)
191p95-I	plain and pale quail, yellow.	(7)
192p95-I	" "	(12)
193p95-I	plain and pale quail, yellow.	(9)
	Normal Abnormal	
	III IO	

Legends :

The figures enclosed in parentheses represent the numbers of egg-batches, the larvae from which were reared in the same lot.

"4m" or "3m" means passing through four or three molts respectively before spinning ("mounting").

The mutants were mated among themselves, and bred true for more than sixteen generations up to the present year. The new strain was named "stick," and has been kept homozygous for the plain marking and the yellow cocoon color. As to the molting character, it has not yet been fixed, but segregates a small percentage of "four-molters," while most of the larvae spin cocoons after three molts, i. e. "three-molters." In order to avoid unfavorable effects, if anything, due to intensive inbreeding, we are keeping the strain in "mixed culture" or rearing the offspring from more than two different mothers, phenotypically alike, in the same lot.

The normals of the lot 193p95-I were also mated inter se, which segregated in mixed cultures a small numbers of "stick" in F_1 , F_2 and F_3 . After F_4 generation no "stick" has appeared in this strain up to F_{11} , when it was discarded.

II. DESCRIPTION OF "STICK" (Plate 2, Figs. 4-6)

The stick silkworm is small and thin in the body-form, and as hard to the touch as a piece of wood. It bends the body apparently with difficulty. Its body-weight, the silk-weight of the cocoon as well as the egg-size are much inferior to the normal as shown in the following tables.

Table 2

Average live weight on the sixth day of the last instar. (Unit gram.)					
Lot No.	Larval characteristics	Average individual weight in gram			
		Normal female	Normal male	Stick female	Stick male
21ah8-2	pY,3m	2.054 (50, ²)	1.552 (50)	1.352 (25)	1.112 (25)
21ah8-3	pY,py,3m	2.034 (50)	1.576 (50)	1.378 (18)	1.115 (20)
21ah8-5	pY,py,3m	1.950 (50)	1.588 (40)	1.250 (9)	0.984 (16)
21ah8-9	pY,3m	1.885(100)	1.445 (70)	1.350 (20)	1.096 (25)
Average		1.981	1.540	1.333	1.077

For the sake of comparison, the figures of the last row in the above table are shown below in percentages, the weight of the normal female being taken as 100.

Normal	Normal	Stick	Stick
♀	♂	♀	♂
100.00	77.73	67.13	54.36

The full-grown larval weight of stick male as represented in percentage of the normal male will be 69.94.

Table 3

Average pupal weight. (Unit gram.)

Weighing was performed in most cases on the tenth day after "mounting."

Lot No.	Larval characteristics	Normal	Normal	Stick	Stick
		♀	♂	♀	♂
20ah8-2	pY,3m	0.855	0.611	0.619	0.461
20bh8-2	pY,3m	0.868	0.643	0.633	0.467
20bh8-3	pY,3m	0.910	0.636	0.628	0.503
20bh8-4	pY,3m	0.811	0.627	0.559	0.463
20ch8-1	pY,4m	1.365(21)	1.027(37)	0.813(12)	0.406(18)
20ch8-3	pY,4m	1.132(23)	0.899(25)	0.780(2)	0.601(8)
20ch8-4	pY,3m	0.875(7)	0.710(45)	0.612(8)	0.516(35)
"	pY,4m	0.924(5)	0.962(33)	0.788(5)	0.708(50)
20ch8-5	pY,3m	0.751(50)	0.620(50)	0.556(46)	0.474(12)
Average		0.943	0.748	0.671	0.511

If we take the normal female as 100.

100.00	79.32	71.16	54.19
--------	-------	-------	-------

The pupal weight of the stick male will, when represented in percentage of the normal male, be 68.31.

² The figures enclosed in parentheses are the numbers of caterpillars weighed.

Table 4

Lot No.	Molting characters	Silk weight. (Unit centigram)			
		Normal ♀	Normal ♂	Stick ♀	Stick ♂
20bh8-2	3m	8.73	8.47	6.01	5.42
20bh8-3	3m	10.51	10.90	7.10	6.45
20bh8-4	3m	9.16	8.51	5.66	5.72
20ch8-1	4m	16.99	16.31	10.17	9.62
20ch8-3	4m	13.00	12.70	9.90	8.50
20ch8-4	3m	10.30(7)	10.11(45)	6.81(8)	5.96(35)
20ch8-4	4m	10.00(5)	14.10(33)	9.20(5)	9.71(50)
20ch8-5	3m	8.35(50)	8.63(50)	6.10(46)	5.94(12)
Average		10.88	11.22	7.62	7.17
Percentage		100.00	103.13	70.04	65.90

Male and female averaged, the ratio of normal and stick as to the silkweight is 100 : 66.92.

We learn from the preceding tables that "stick" is less heavy in live-weight than the normal larvae by 30 to 35%, and produces silken substance corresponding to 67% of the normal in average.

Stick grows slower and experiences some difficulty in shedding the old skin in molt. Usually a greater proportion of stick is lost during the larval life when stick and normal fed together on the same tray.

The characteristics are not striking in younger stages of the larva, and in the beginning period even in later instars, i. e. within two or three days after ecdysis. They are most easily appreciable just before a molt or before "mounting." The stick silkworm resembles "stony"³ and "constricted"³ so far as the body stiffness is concerned, but the former differs in being smooth on the body surface while the two latter have bodies segmentally constricted so that they remind us of a piece of bamboo.

III. MULTILUNAR (Plate 2, Figs. 7-9.)

This marking consists of a series of pairs of large, brown, rounded spots that develop after the first molt on the dorsal surface of the abdominal segments. As to the hereditary behavior of this marking, it has already been described by ISHIWATA and ARAKI (1902-1905), TOYAMA

3 These characters will be described elsewhere

(1908-1909), especially in detail by one of us (TANAKA 1916). But no linked gene with this marking has yet been known.

IV. NORMAL x STICK

1) F_1 generation.

This crossing was made reciprocally, ten batches of F_1 eggs hatched and were reared. All F_1 caterpillars, in a total of 2483, were normal indistinguishable from pure normals. Stick is a complete recessive to normal.

2) F_2 generation.

The F_2 larvae from different egg-batches were reared in separate lots, and counted when full-grown. The result follows:

Table 5

P	Lot No.	Normal	Stick	Totals
Normal ♀ x Stick ♂	203h813	178	60	238
"	203h814	134	34	168
"	203h815	155	44	199
"	203h816	124	51	175
"	203h817	222	60	282
"	203h818	90	27	117
"	211h824	166	53	219
"	222h826	73	34	107
"	222h261	57	33	90
Stick ♀ x Normal ♂	203h81	281	90	371
"	203h82	203	64	267
"	203h89	158	56	214
"	203h811	120	33	153
"	203h814	149	40	189
"	203h820	87	32	119
"	203h821	210	52	262
"	222h819	25	11	36
"	222h820	129	35	164
"	222h821	111	34	145
"	222h822	103	40	143
Totals		2775	883	3658
Expectation		2743.5	914.5	
Deviation		+31.5	-31.5	
Standard deviation		±26.19	±26.19	

Thus 3 : 1 ratio has evidently been realised.

3) Back-crossing.

Table 6

Mating	Lot No.	Normal	Stick	Total
F ₁ ♀ x stick ♂	202h84	102	85	187
"	203h84	191	197	388
"	203h85	201	170	371
Stick ♀ x F ₁ ♂	202h83	75	71	146
"	203h86	82	60	142
Totals		651	583	1234
Expectation		617	617	
Deviation		+ 34	- 34	
Standard deviation		± 17.57	± 17.57	

The deviation is not larger than twice the standard deviation, so that the experimental result is not inconsistent with a 1 : 1 ratio as expected.

V. LOWER PROPORTION OF SURVIVORS IN STICK

From the results mentioned above, we learn that stick is due to a simple recessive mutation which occurred in the pedigree in a stage some previous to the autumn 1919. The fact that the experimental numbers of stick always face below the theoretical expected numbers, though not far below, is not merely accidental, but is owing to the inferior viability or lesser powers of survival. This is partly due to general weakness of the mutant and partly to its retarded growth, thus making stick more likely to be lost in the course of rearing. How many sticks are lost depends on environmental conditions. If 5% of the numbers of survived sticks is added to the results given in tables 5 and 6, the ratios will come very close to the expected as follows:

Table 7

		Normal	Stick	Totals
F ₂	Actual numbers	2775	883	3658
	Corrected numbers	2775	927	3702
	Theoretical numbers	2776.5	925.5	
	Deviation	- 1.5	+ 1.5	
	Standard deviation	± 26.3	± 26.3	
Back cross	Actual numbers	651	583	1234
	Corrected numbers	651	612	1263
	Theoretical numbers	631.5	631.5	
	Deviation	+ 19.5	- 19.5	
	Standard deviation	± 17.8	± 17.8	

VI. SYMBOLS

The mutant stick will be represented by sk , and its normal allelomorph by Sk . That the symbols for Multilunar and its normal gene are L and l respectively is shown in a previous paper by one of us (TANAKA 1916).

VII. CROSSING-OVER VALUE

All hybrid individuals produced by crossing $L \times sk$, in a total of 1664, were Multilunar normal.

In F_2 , four possible classes, Multilunar normal ($\bar{L} Sk$), Multilunar stick ($L sk$), not-Multilunar normal ($l Sk$) and not-Multilunar stick ($l sk$), have appeared in a ratio remarkably different from 9 : 3 : 3 : 1, showing evidently a linkage relation between L and sk .

Table 8

P	F_2 lot No.	L Sk	L sk	l Sk	l sk	Totals
1. ♀ x sk ♂	223s11	52	5	4	13	74
"	223s12	54	0	2	20	76
"	223s13	64	0	3	11	78
"	223s14	47	5	2	18	73
"	223s15	201	6	13	47	267
sk ♀ x L ♂	224h831	235	23	22	61	341
"	224h832	253	21	38	52	364
"	224h833	220	18	19	38	295
"	224h834	188	19	20	46	273
"	224h835	151	14	16	36	217
"	232l441	163	12	10	32	217
"	232l442	187	15	14	35	251
"	232l443	170	14	16	33	233
"	232m44	113	14	13	28	168
Totals		2099	166	192	470	2927

The crossing-over value calculated from the preceding result is 24.47 %.

Mating double recessives and F_1 dihybrids.

$$a) \frac{1 sk}{1 sk} \text{ ♀ } \times \frac{L Sk}{1 sk} \text{ ♂ }$$

Table 9

P	Lot No.	L Sk	L sk	l Sk	l sk	Total
L Sk ♀ x l sk ♂	2321411	37	24	16	37	114
"	2321412	47	23	22	35	127
"	2341413	68	26	26	60	180
"	2341414	59	31	21	58	169
"	2341415	46	20	27	39	132
"	2321416	67	19	26	53	165
"	2321417	64	16	19	43	142
"	2321418	45	15	13	47	120
"	2321419	59	16	17	48	140
"	2321420	47	13	8	34	102
"	2321421	63	32	23	73	191
"	2321422	52	23	30	55	160
"	2321423	59	14	15	46	134
"	2321424	59	12	14	55	140
"	2321425	48	23	17	33	121
sk ♀ x L ♂	233145	68	21	34	77	200
"	2331451	23	10	18	39	90
"	2331452	69	13	20	72	174
"	2331453	55	26	32	79	192
Totals		1035	377	398	983	2793

$$b) \frac{1 \text{ sk}}{1 \text{ sk}} \text{ ♀ } \times \frac{L \text{ sk}}{1 \text{ Sk}} \text{ ♂ }$$

l Sk ♀ x L sk ♂	244151	104	308	319	103	834
(mixed culture)						

Thus there were 982 cross-overs altogether among 3627 individuals, which correspond to 27.07% of the total. Averaging F_2 and back-cross results we get 25.77%. The differential survivorship mentioned does not affect the crossing over value at all.

$$c) \frac{L \text{ Sk}}{1 \text{ sk}} \text{ ♀ } \times \frac{1 \text{ sk}}{1 \text{ sk}} \text{ ♂ }$$

The heterozygous females were tested by mating them to the double recessive males, and only two phenotypes were obtained as expected. There occurs no crossing-over in the female sex as in other cases of linkage in *Bombyx*.

Table 10

Lot No.	L Sk	L sk	l Sk	l sk	Total
2421431	131	0	0	130	261
2421432	142	0	0	129	271
2421433	184	0	0	203	387
Totals	457	0	0	462	919
Expected	459.5	0	0	459.5	

The actual numbers accord exactly with the expectation, without any correction, owing, perhaps, to favorable conditions.

VIII. SUMMARY AND CONCLUSION

a) *Stick* appeared as a simple recessive mutation in the third season culture of 1919. The family in which the mutants were discovered was F_{10} generation of a hybrid between a Japanese bivoltine white (four molts, pale-quail marking) and a Chinese univoltine yellow (three molts, plain-skinned).

b) The body of the *stick* caterpillar is thin and stiff and is easily distinguishable from normal by inspection. The growth of *stick* is always slower than that of normal.

c) A greater percentage of *stick* is lost during the larval development than of normal. This accounts for the deficient numbers of *sticks* observed in experiments. The survivorship of *stick* is inferior to normal roughly by 5%. The differential viability is however, scarcely noted in favorable conditions.

d) *Multilunar* and *stick* are linked in inheritance, and the crossing-over between them is proved to be about 25.8%. It has been shown that *Multilunar* is inherited independently from the genes of the first, second and third linkage groups (TANAKA 1916, 1922, OGURA 1922), thus it forms, with *stick*, a fourth linkage group in the silkworm.

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EXPLANATION OF PLATE 2

- Figs. 1-3. Normal. (1 Sk)
 Figs. 4-6. *Stick*. (1 sk)
 Figs. 7-9. *Multilunar*. (L Sk)
 Figs. 10-12. *Multilunar stick*. (L sk)

Note :—No. 7 is in a contracted state of the body in contrast to No. 10 which shows the body fully extended. This is why the former is seen to be smaller than the latter.



SOME REMARKS ON SYMBOLS, MULTIPLE ALLELOMORPHISM, CROSSING OVER AND LINKAGE GROUPS IN THE SILKWORM¹

Yoshimaro TANAKA

I. REVISION OF SYMBOLS FOR TWO LARVAL MARKINGS

According to the nomenclature of genes in *Drosophila*, a recessive mutation is to be represented by a small letter or letters significant to the mutated character, and its normal allelomorph by the corresponding capital letter with or without the suffix of the small letters. Since 1917 I have followed this method of nomenclature, though a different scheme was used in my earlier works. For instance, the plain marking was represented by P, to which q was added whenever necessary to distinguish the plain from normal. Thus it is actually not P or p that distinguishes the plain from the other markings. This is at least confusing if not absurd especially when there are many recessive genes affecting the same organ as already pointed out by MORGAN (1913). It seems, therefore, desirable to revise the symbols for recessive larval markings, i. e. plain and quail. To make clear the history of changes, the symbols are listed below:

	Papers	Normal	Plain	Quail	Pale quail
TANAKA	1913a, b. 1914. 1915.	N	n	—	—
TANAKA	1916.	PQ	Pq	pQ	pq
	New symbols	PQ	p	q	pq
	Consequently,				
		Striped	Moricaud	Striped quail	Moricaud quail
TANAKA	1916.	SPQ	MPQ	SpQ	MpQ
	New symbols	S	M	Sq	Mq

¹ Contributions from the Sericultural Laboratory, Kyushu Imperial University. No. 10.

Bombyx mori has been domesticated for thousands of years, and no one can tell exactly the origin of our silkworms, though the wild mulberry silkworm is generally presumed to be their ancestral form. The wild mulberry silkworm is sometimes called *Theophila mandarina*, and sometimes *Bombyx mandarina*, but *Bombyx mori* var. *mandarina* seems to me better fitting as its scientific name. Besides the unsettled systematic position, the genetic characters of the wild silkworm are not yet fully worked out. It seems, therefore, more convenient, in *Bombyx*, to take the more common type as the standard, and the less common form as the mutant as BRIDGES and MORGAN propose (1923) for the cases where the wild type is unknown or not certainly known. Some important standard characters are compared to those of *mandarina*.

	Standard form of <i>B. mori</i>	<i>Mandarina</i> form
Larval marking	Normal	Moricaud
Blood color	Colorless	Light yellowish
Cocoon color	White	Light green
Voltinism	Univoltine	Polyvoltine
Number of molts before spinning	Four	Four
Skin	Opaque	Opaque

Determination of the standard form may sometimes be arbitrary, because we can not say which larval marking, "normal" or "plain," for example, is really more common in the world. It is, however, true that we can pick the more common type as the standard without difficulty in majority of cases.

II. MULTIPLE ALLELOMORPHISM

Special relations between four larval markings, striped, moricaud, normal and plain described in my previous papers (1913b, 1914) were pointed out by STURTEVANT (1915) as they form a series of multiple allelomorphs. Though I adopted the explanation by complete coupling and repulsion in my paper of 1916 as I did in the preceding work, I have later accepted the idea of multiple allelomorphism for this case. The students of *Drosophila* make use of exponents to denote multiple allelomorphs, as w^e , e^s etc. for example. But I am, for the time being, content with the use of the simpler expressions, S (striped) and M (moricaud) instead of symbols p^s and p^m .

III. CROSSING OVER VALUE

It may be somewhat useful that the phenotypic ratios published in my previous paper (1916) to be expressed in terms of the crossing over

value. As there is no crossing over in the female sex in *Bombyx*, the cross over value in diheterozygous males may be calculated from F_2 results by the following formula, in which k , l , m and n represent the numbers of individuals belonging to AB, Ab, aB and ab F_2 phenotypes.

$$\text{Cross-over value} = 1 \div \left\{ \frac{k + n}{2(l + m)} + 0.5 \right\} \times 100$$

This formula is available for F_2 ratios in "coupling" only, while in case of "repulsion" the F_2 ratio is uniformly 2 : 1 : 1 whatever the linkage value may be (TANAKA 1916), which makes calculation of cross-over per cents impossible. The crossing over per cents are to be obtained only through back-crossing, when two dominants are introduced from different parents.

a) Striped-yellow linkage.

	SY	Sy	sY	sy	Totals	c.o. %
"Coupling" { Back cross	4421	1631	1735	4418	12205	27.58
{ F_2	10958	1075	1101	3017	16151	26.95
"Repulsion" (back cross)	112	338	372	119	941	24.55
Weighted mean of c.o.						27.22

b) Moricaud-yellow linkage.

	MY	My	mY	my	Totals	c.o. %
"Coupling" { Back cross	3053	1030	1057	3129	8269	25.24
{ F_2	10512	873	858	2949	15192	22.78
"Repulsion" (back cross)	86	453	483	104	1126	24.02
Weighted mean of c.o.						23.66

c) Plain-yellow linkage.

	PY	Py	pY	py	Totals	c.o. %
"Coupling" { Back cross	719	207	186	614	1726	22.77
{ F_2	3361	376	294	910	4941	27.12
"Repulsion" (back cross)	280	827	756	222	2085	24.08
Weighted mean of c.o.						25.54

As the genes S,M and p are multiple allelomorphs, they ought to be all the same in cross over percentage, but there is actually remarkable deviation from expectation. This is, however, not astonishing when we take into consideration the fact that very different numbers were obtained from back-crossing and F_2 results even between the same genes. For instance, crossing over value calculated from back-crossing in p-Y linkage is 22.77, while that derived from F_2 figures is 27.12, showing a difference of 4.35%. KOGURE (1926) studied, in my laboratory, on the crossing over variation between S and Y, and discovered the existence of a

dominant modifier which partly suppresses crossing over between them and reduces it as low as 12%. He finds also that the crossing over percentage is influenced by the room temperature where the heterozygotes were reared: the average crossing over value of his "high crossing over" strain was 21.48 in about 30° C, while it was 25.86% in about 19°C, and some intermediate figures were obtained in intermediate thermometric degrees. The weighted mean of cross-over per cents between Y and the locus of p, S,M is 25.6 in my experiments.

IV. LINKAGE GROUPS AND CHROMOSOME MAPS

Four linkage groups have hitherto been described in the silkworm. They are as follow:

Linkage groups or chromosomes	Genes contained	Authors
I (Sex-chromosome)	os	TANAKA (1921), NISHIKAWA (1922)
	e	TANAKA (1924)
	od ²	TANAKA (1926)
II	S,M,p,Y	TANAKA (1913b, 1914, 1915, 1916)
III	Z,I	OGURA (1922)
IV	sk,L	TANAKA and MATSUNO (1927)

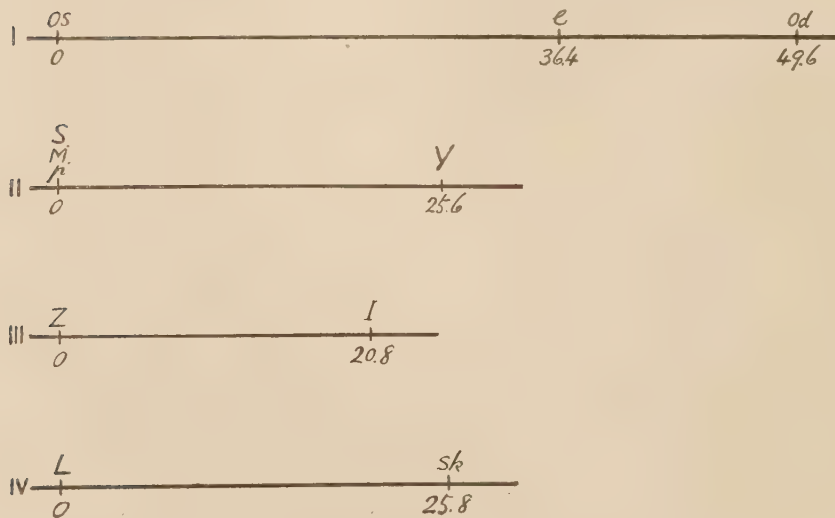


Fig. 1.

Chromosome maps I to IV in the silkworm.

² The description in English will soon appear.

A few more possible cases of linkage are known to me at present, but they have not been fully worked out.

The chromosome maps of the silkworm are drawn on basis of published data, taking the cross-over per cents as units as such.

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